

CC -I- SIMILARITY: Contains 1 RNase III domain.  
CC -----  
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CC -----

Query Match 89.1%; Score 1017; DB 2; Length 226;  
Best Local Similarity 87.2%; Pred. No. 7.6e-73;  
Matches 197; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MEPIKNLPRLCRTLGYEFNNIELLIQALTHRSAANKHNERLEFLGDSILSIAISDALYHQ 60  
|||||

**Qy**      61 FPKATEGDLRMRATLVKGGDTLTIIAKKEFKLGDYLYLGPGELKSGGGERRESILADAVEAI 120  
         |||||::|||||:  
**Dd**      61 FPKATEGDLRMRATLVRGDDTLTIIAQQEKLGDYLYLGPGELKSGGGERRESILADAVEAI 120

**Qy**            121 IGAVYLDADIEVCRKLLLSWYQERLAEIKPGINKDKPTILQEVLQGFKKLPLDYOVWAV 180  
               |||||:::||::|||::||::||::||::||::||::||::||::||::||::||::||::||  
**Dd**            121 IGAVYLDSDLEVCRAILLKKWAERLAEIOPGISOKDAKTILLEHLOGFKKLPLDYOVINI 180

Qy 181 EGEAHDQTFTVECKISELDKVVTVGVASSRRKAEDLAAQVLELLNK 226  
::|:|||||::|:|:| | |||||::|:||||| |

Dd 181 EGDAHDTFTVECRDLSOSVIGVASSRRKAEDIAAQWLELLKK 226

### RESULT 13

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ID   RWC_SHEON                      Reviewed:              226 AA.
AC   Q9H9H1;
DT   21-MAR-2006, integrated into UniProtKB/Swiss-Prot.
DT   01-MAR-2005, sequence version 1.
DT   24-JUL-2007, entry version 26.
DE   Ribonuclease 3 (EC 3.1.26.3) (Ribonuclease III) (RNase III).
GN   Name=rnc; ORF=locusNames=Q9_1346;
OS   Shewanella oneidensis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Altrapomondales;
OC   Shewanellaceae; Shewanella.
NC   NCBI_TaxID=70863;
RN   [1]
RF   NUCLEOTIDE SEQUENCE [Large Scale Genomic DNA].
RC   STRAIN=WF-1.
RX   MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RA   Heidelberg J.F., Paulsen T.J., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA   Read T.D., Eisen J.A., Seshadri R., Ward N.L., Mathe A.B.,
RA   Clayton R.A., Wayer T., Taplin A., Scott J., Beaman M.J.,
RA   Brinkak L.M., Daugherty S.C., Dobby R.T., Dodson R.J., Durkin A.S.,
RA   Haft D.H., Kolonay J.F., Madupu R.P., Peterson J.D., Umayam L.S.,
RA   White C., Wolf A.M., Vamathean J.C., Weidman J.F., Ispahani M.,
RA   Lee K., Berry K.R., Lee C., Mueller J., Shouri H.M., Gill J.,
RA   Utterback R.N., McDowell L., Delabybay N.V., Smith H.O.,
RA   Venter J.C., Nelson K.E., Fraser C.M.
RT   "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT   Shewanella oneidensis."
RL   Nat. Biotechnol. 20:1118-1123 (2002).
CC   -!- FUNCTION: Digests double-stranded RNA. Involved in the processing
CC   of ribosomal RNA precursors and of some mRNAs (By similarity).
CC   -!- CATALYTIC ACTIVITY: Endonuclease cleavage to 5'-
CC   phosphomonoester.
CC   -!- SUBCELLULAR LOCATION: Cytoplasm (By similarity).
CC   -!- SIMILARITY: Contains 1 DSBM (double-stranded RNA-binding) domain.

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DR EMBL; J014239; RANW5411.1; -. ; Genomic_DNA.
DR HSSP; QXW016; 100K.
DR GenomeReviews; J014239_GR; S01348.
DR KEGG; scm:S01348; -.
DR TIGR; S01348; -.
DR BioCyc; SWE211566:S01348-MONOMER; -.
DR GO; GO:0004525; F:ribonuclease III activity; IEA:HAMAP.
DR GO; GO:0006397; P:mRNA processing; IEA:HAMAP.
DR GO; GO:0006364; P:rRNA processing; IEA:HAMAP.
DR HAMAP; MF_00104; -. 1.
DR InterPro; IPR001159; ds_RNA_bd.
DR InterPro; IPR014720; dsRNA-bd-like.
DR InterPro; IPR000399; RNase_III.
DR InterPro; IPR011907; RNase_III_bac.
DR Gene3D; G3DSA.3.30.160.20; dsRNA-bd-like; 1.
DR Gene3D; G3DSA.1.10.1520.10; RNase_III; 1.
DR Pfam; PF00035; dsrm; 1.
DR Pfam; PF07636; Ribonuclease_3; 1.
DR SMART; SMO0358; DSRM; 1.
DR SMART; SMO0355; RIBCO; 1.
DR TRSGFams; TIGR02191; RNaseIII; 1.
DR PROSITE; PS50137; DS_RBD; 1.
DR PROSITE; PS00517; RNASE_3_1; 1.
DR PROSITE; PS50142; RNASE_3_2; 1.
FE 3: Inferred from homology.
KM Complete proteomes; Cytoplasm; Endonuclease; Hydrolase; Nuclease;
KM RNA-binding.
FT CHAIN 1 226 Ribonuclease 3.
FT /FTID=PRO_0000228573.
FT DOMAIN 7 123 RNase III.
FT DOMAIN 156 226 DSRM.
SQ SEQUENCE 226 Aa; 25329 Nw; 77722568BC0C12C5 C864;

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Query Match 88.7%; Score 1012; DB 1; Length 226;  
Best Local Similarity 85.44; Pred. No. 1.9e-72;  
Matches 193; Conservative 20; Mismatches 13; Indels 0; Gaps 0;

Qy 1 MEPIKNLPRLCRTLGYEFNNIELLQALTHRSAANKHNERLEFLGDSILSIAISDALYHQ 60  
|||||::|

**Qy**      61 FPKATEGDLSRMRA TLVKGDTLTIIAKEFKLGDYLYLPGE LKSGGFRR ESILADAVEAI 120  
         ||||| : | : | : |  
**Ry**

**Qy** 121 IGAVYLDADIEVCRKLLLSWYQERLAEIKPGINQKDPKTLQEYLQGFKPLPDYQVVAV 180  
||::|::|:||||:||||:| |||||:||||| |::||| |||||:::

Qy 181 EGEAHDQTFTECKISELDKVVTVGVASSRRKAEQLAAQVLELLNK 226  
||:|||||||:|:|:| |||||||:||||||| |

Db 181 EGDHDDQTFTECRIDDISQSVIGVASSRRKAEQIAAAQVLELLK 226